Amendments to the Specification:

Please replace the paragraph beginning on page 8, line 23, with the following amended paragraph:

Methods of aligning sequences for comparison are well known in the art. Gene comparisons can be determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., *et al.*, (1993) *J. Mol. Biol.* 215:403-410[[;]] ~~see also www.ncbi.nlm.nih.gov/BLAST~~) searches under default parameters for identity to sequences contained in the BLAST "GENEMBL" database. A sequence can be analyzed for identity to all publicly available DNA sequences contained in the GENEMBL database using the BLASTN algorithm under the default parameters. Identity to the sequence of the present invention would mean a polynucleotide sequence having at least 65% sequence identity, more preferably at least 70% sequence identity, more preferably at least 75% sequence identity, more preferably at least 80% identity, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity and most preferably at least 95% sequence identity wherein the percent sequence identity is based on the entire promoter region.

Please replace the paragraph beginning on page 21, line 18, with the following amended paragraph:

Once positive BACs were identified, a southern analysis using a HindIII digestion was performed on them to identify bands containing Lec1 for subcloning. The same probe was used to identify a fragment (~4kb) which was positive for Lec1. This band was subcloned into the pBS2KS+ cloning vector (Stratagene Inc., 11011 N. Torrey Pines Rd., La Jolla, CA[[;]] ~~www.strategene.com~~) and sequenced. The band contained 1.4 kb of sequence upstream of the coding region of Lec1 and 1.7 kb of sequence downstream. The Lec1 promoter and terminator regions were obtained using primers SEQ ID NOS: 17, 18, 19 and 20, created from this sequence

to amplify genomic DNA from maize line A63. The PCR reaction was performed in a Bio-Rad icycler (Hercules, CA) thermal cycler using Hifidelity supermix (Cat.# 10790-020, Life Technologies, Rockville Maryland). The following cycle parameters were used: 94°C for 2 seconds, followed by 30 cycles of 94°C for 20 seconds, 58°C for 30 seconds, and 68°C for 1 minute. Finally, the samples were held at 67°C for 4 minutes and then at 4°C until further analysis. The PCR products were then cloned into the pGEM-T Easy vector (Promega Corp. Madison, WI). Clones were sequenced for verification.

Please replace the paragraph beginning on page 22, line 2, with the following amended paragraph:

Promoter::GUS fusion constructs were prepared by the methods described below. All vectors were constructed using standard molecular biology techniques (Sambrook et al., Supra). A reporter gene and a selectable marker gene for gene expression and selection was inserted between the multiple cloning sites of the pBluescript cloning vector (Stratagene Inc., 11011 N. Torrey Pines Rd., La Jolla, CA[[;]] ~~www.strategene.com~~). The ampicillin resistance gene was replaced with a kanamycin resistance gene to allow use in bombardment experiments. The reporter gene was the β-glucuronidase (GUS) gene (Jefferson, R.A. *et al.*, 1986, Proc. Natl. Acad. Sci. (USA) 83:8447-8451) into whose coding region was inserted the second intron from the potato ST-LS1 gene (Vancanneyt *et al.*, Mol. Gen. Genet. 220:245-250, 1990), to produce GUSINT, in order to prevent expression of the gene in Agrobacterium (see Ohta, S. *et al.*, 1990, Plant Cell Physiol. 31(6):805-813. A fragment containing bases 2 to 310 from the terminator of the potato proteinase inhibitor (pinII) gene (An *et al.*, *Plant Cell* 1:115-122, 1989) was blunt-end ligated downstream of the GUS coding sequence, to create the GUS expression cassette. The 3' end of the terminator carried a NotI restriction site. The respective promoter regions were ligated in frame to the NcoI site 5' to the GUS gene at the start codon.